

SEQ ID NO:1

1 ggaattccgg ctataggcag aggagaatgt cagatgccta gctcggtccc ctccgcctga
 61 cgctcctctc tgtctcagcc aggactggtt tctgtaagaa acagcaggag ctgtggcagc
 121 ggcgaaagga agcggctgag gcgcttggaa cccgaaaagt ctccgtgctc ctggctaccc
 181 cgcacagcgg tgcccccccg gccgtcagta ccatggacag cagcgctgcc cccacgaacg
 241 ccagcaattt cactgatgcc ttggcgtact caagttgctc cccagcaccc agccccggtt
 301 cctgggtcaa cttgtcccac ttagatggca acctgtccga cccatgcggc ccgaaccgc
 361 ccaaacctggg cgggagagac agcctgtgcc ctccgaccgg cagtccctcc atgatcacgg
 421 ccatcacgat catggccctc tactccatcg ttgtcgtggt gggctcttc ggaaacttcc
 481 tggtcatgtt tggattgtc agatacacca agatgaagac tgccaccaac atctacatTT
 541 tcaacacctgc tctggcagat gccttagcca ccagtagccct gccttccag agtgtgaatt
 601 acctaataatggg aacatggcca tttggAACCA tcctttgcaa gatagtgtatccatagatt
 661 actataaataat gttcaccaggc atattcaccc tctgcacccat gagttgtat cgatacattt
 721 cagtctgcca ccctgtcaag gccttagatt tccgtactcc cccggaaatgccc aaaattatca
 781 atgtctgcaa ctggatccctc tcttcagcca ttggcttccatcc tggatgttcc atggctacaa
 841 caaaaatacag gcaagggttcc atagattgtat cactaacatt ctctcatcca acctggact
 901 gggaaaaaccc tggtaagatc tggatTTCA tcttcgcctt cattatgcca gtgtcatca
 961 ttaccgtgtg ctatggactg atgatcttgc geetcaagag tggccatcg ctctctggct
 1021 cccaaagaaaa ggacaggaaat cttcgaagga tcaccaggat ggtgctgggt gtggggct
 1081 tggatgtatcg tggatggact cccattcaca tttagtgcat cattaaagcc ttgggttacaa
 1141 tcccgaaaac tacgttccatc actgttttcc tggcacttctt cattgtctca ggttacacaa
 1201 acagctgcct caacccagtc ctttatgtat ttctggatga aaacttcaaa cgatgttca
 1261 gagagttctg tatcccaacc tcttccaaca ttgagcaaca aaactccact cgaattcgcc
 1321 agaacactag agaccacccc tccacggcca atacagtggat tagaactaat catcagctag
 1381 aaaatctgga agcagaaact gctccgttgc ccttaacaggg tctcatgcca ttccgaccc
 1441 caccaagctt agaagccacc atgtatgtgg aagcagggtt cttaagaat gtgttaggagg
 1501 ctctaattct ctagggaaatgt gcctactttt aggtcatccaa accttttcc tctctggcca
 1561 ctctgctctg cacatttagag ggacagccaa aagtaagtgg agcatttggaa aggaaaggaa
 1621 tataccacac cgaggagttc agtttgcata agacacccat tggaaacccaa acccatcgat
 1681 gtatgtgaat tgaagtcatc ataaaagggtt acccttctgt ctgtaaat ttatTTCAA
 1741 gcaaatatTTT atgacccatcaa caaagaagaa ccatttttgc ttaagttcac cgttagtaaca
 1801 cataaagttaa atgctaccc tgcataaaggc accttgcattt gaagggtccga gtcttttag
 1861 tggatgttgc aaggaaatgaa tccattattt tatttttagac ttttaacttca aacttttttt
 1921 tagcatctgg ctaaggcatc attttccatc ccatttttgc tttttgtatt gtttttttttt
 1981 aataacatct ctttcatcta gctccataat tgcaaggaa gagatttagca tgaaaggtaa
 2041 tctgaaacac agtcatgtgt canctgttaga aagggttattt cttcatgcact ncaaataactt
 2101 ccaagagtc atcatggggg atttttcattt ctttaggctt cagtggttttgc ttccctggaaat
 2161 tc

DRAFT DRAFT DRAFT DRAFT

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FIGURE 1B

SEQ ID NO:2

Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
1 5 10 15
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val
20 25 30
Asn Leu Ser His Leu Asp Gly Asn Leu Ser Asp Pro Cys Gly Pro Asn
35 40 45
Arg Thr Asn Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
50 55 60
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
65 70 75 80
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
85 90 95
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
100 105 110
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val
115 120 125
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile
130 135 140
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu
145 150 155 160
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys
165 170 175
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys
180 185 190
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala
195 200 205
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser
210 215 220
His Pro Thr Trp Tyr Trp Glu Asn Leu Val Lys Ile Cys Val Phe Ile
225 230 235 240
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu
245 250 255
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu
260 265 270
Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
275 280 285
Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
290 295 300
Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
305 310 315 320
His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
325 330 335
Leu Tyr Ala Phe Leu Asp Glu Asn Phe Arg Cys Phe Arg Glu Phe
340 345 350
Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
355 360 365
Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
370 375 380
Thr Asn His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
385 390 395 400

SEQ ID NO:3

1 ggaattccgg ctataggcg aggagaatgt cagatgctca gtcgggtccc ctccgcctga
61 cgctcctctc tgtctcagcc aggactgggt tctgtaaagaa acagcaggag ctgtggcagc
121 ggcgaaaaggaa agcggctgag ggcgttggaa cccgaaaaagt ctcggtgctc ctggctaccc
181 cgcacagcgg tgccccccg ggcgtca gcatggacag cagcgtgtgcc cccacgaacg
241 ccagcaattt cactgtatgcc ttggcgtaact caagttgcgc cccagcaccc agccccgggt
301 cctgggtcaa cttgtccac tttagatggca acctgtccga cccatgcggg cccgaaccgca
361 ccaacctggg cgggagagac agcctgtgcc ctccgaccgg cagtcctcc atgatcacgg
421 ccatcacgt catggccctc tactccatcg tgtgcgttgtt ggggcttcc ggaaacttcc
481 tggtcatgtt tggattgtc agatacacca agatgaagac tgccaccac atctacattt
541 tcaacccctgc tctggcgat gccttagcca ccagttccctt gcccttccag agtgtgaatt
601 acctaattggg aacatggca ttggaaacca tcctttgcaaa gatagtgtatccatagatt
661 actataacat gttcaccaggc atattcaccc tctgcaccat gaggtgttatcgatcattt
721 cagtcgtccca ccctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca
781 atgtctgcaat ctggatccctc tttcagcca ttggcttcc tgaatgttca atggctacaa
841 caaaatacag gcaagggttcc atagattgttca cactaacatt ctctcatcca acctggact
901 gggaaaacctt cgtgaagatc tggattttca tcttcgctt cattatgcca gtgctcatca
961 ttaccgtgtt ctatggactg atgatcttgc gcctcaagag tgccgcgtt ctctctggct
1021 ccaaagaaaa ggacaggaat ctgcgaaggat tcaccaggat ggtgttgtt gtggggctg
1081 tggtcatcgat ctgctggact cccatttcaca tttacgtcat cattaaagcc ttggtttacaa
1141 tccccagaaac tacgttccag actgttttctt ggcacttctg cattgtctca ggttacacaa
1201 acagctgcctt caacccagtc ctttatgtat ttctggatga aaacttcaaa cgatgcttca
1261 gagagttctg tatcccaacc tttccaaca ttgagcaaca aaactccact cgaattcgct
1321 agaacacttag agaccaccccc tccacggca atacagtgg tagaaactaat catcagctag
1381 aaaatctggaa agcagaaaact gtcgggttgc ccttaacagggtt tctcatgcca ttccgaccc
1441 caccaagctt agaaggccacc atgtatgtgg aagcagggtt cttcaagaat gtgttaggagg
1501 ctcttaattctt ctagaaaagt gcctactttt aggtcatcca acctcttcc tctctggcca
1561 ctctgtctgtt cacatttagag ggacagccaa aagtaagtgg agcattttggaa agggaaaggaa
1621 tataccacac cgaggagtcc agtttgcata agacacccag tggaaacccaa acccatcgat
1681 gtatgtgaat tgaagtcatc ataaaaggtt acccttctgt ctgttaagatt ttattttca
1741 gcaaataattt atgacctcaaa caaagaagaa ccatcttttgc ttaagttcac cgttagtaaca
1801 cataaaagttaa atgctaccc tgcataaaggc accttgaatg gaaggtccga gtcttttag
1861 tggggatggca agggaaatgaa tccattatttgc tatttttagac ttttaacttc aactttaaaat
1921 tagcatctgg ctaaggcattt atttcaccc tccatcttgc gttttgtatt gttttaaaaaa
1981 aataacatctt ctttcatctt gtcctataat tgcaaggaa gagatttagca tgaaaggtaa
2041 tctgaaacac agtcatgtgt canctgttgc aaggttgatt ctcatgcact ncaaataactt
2101 ccaaagagtc atcatggggg atttttcattt ctttaggtttt cagtggttttgc ttccctggaaat
2161 tc

600-1-266P
SEQ ID NO:4

FIGURE 2B

Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
1 5 10 15
Leu Ala Tyr Ser Ser Cys Pro Pro Ala Pro Ser Pro Gly Ser Trp Val
20 25 30
Asn Leu Ser His Leu Asp Gly Asn Leu Ser Asp Pro Cys Gly Pro Asn
35 40 45
Arg Thr Asn Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
50 55 60
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
65 70 75 80
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
85 90 95
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
100 105 110
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val
115 120 125
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile
130 135 140
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu
145 150 155 160
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys
165 170 175
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys
180 185 190
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala
195 200 205
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser
210 215 220
His Pro Thr Trp Tyr Trp Glu Asn Leu Val Lys Ile Cys Val Phe Ile
225 230 235 240
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu
245 250 255
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu
260 265 270
Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
275 280 285
Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
290 295 300
Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
305 310 315 320
His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
325 330 335
Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
340 345 350
Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
355 360 365
Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
370 375 380
Thr Asn His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
385 390 395 400

SEQ ID NO:5

1 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcggtccc ctccgcctga
61 cgctcctctc tgtctcagcc aggactgggt tctgtaaagaa acagcaggag ctgtggcagc
121 ggcgaaagga agcggctgag ggcgttggaa cccgaaaagt ctcgtgctc ctggctaccc
181 cgcacagcgg tgcccgcccc ggcgtcagta ccatggacag cagcgtgcc cccacgaacg
241 ccagcaattg cactgatgcc ttggcgtact caagttgctc cccagcaccc agccccgggt
301 cctgggtcaa cttgtccac tttagatggca acctgaccga cccatgcggg ccgaaccgca
361 ccaacctggg cgggagagac agcctgtgcc ctccgaccgg cagttccctcc atgatcacgg
421 ccatcacgt catggccctc tactccatcg tgcgttggt ggggtcttc ggaaacttcc
481 tggcatgta tgcgttgc agataccca agatgaagac tgccaccaac atctacatt
541 tcaaccttgc tctggcagat gccttagcca ccagtacccct gcccttccag agtgtgaatt
601 acctaattggg aacatggcca tttggaacca tcctttgcaa gatagtgtac tccatagatt
661 actataaacat gttcacccat atattcaccc tctgcacccat gagttgtat cgatacatttgc
721 cagtcgtcca ccctgtcaag gccttagatt tccgtactcc ccgaaatgcc aaaattatca
781 atgtctgcaa ctggatcctc tcttcagcca ttggcttcc tgtaatgttc atggctaccaa
841 caaaatacag gcaagggttcc atagattgt aactaaccatt ctctcatcca acctggtaact
901 gggaaaacct cgtgaagatc tgcgtttca tcttcgcctt cattatgcca gtgcgtatca
961 ttaccgtgtc ctatggactg atgatcttgc gcctcaagag tgcgtccatg ctctctggct
1021 caaaaagaaaa ggacaggaat cttcgaagga tcaccaggat ggtgcgtgtg gtggggctg
1081 tggcatcgat ctgcgtggact cccattcaca ttacgtcat cattaaagcc ttggttacaa
1141 tcccgaaaac tacgttccag actgtttctt ggcacttctg cattgtctca gtttacacaa
1201 acagctgcct caacccagtc ctttatgcat ttctggatga aaacttcaaa cgatgcttca
1261 gagagttctg tatcccaacc tcttcaca ttgagcaaca aaactccact cgaattcgct
1321 agaacactag agaccacccc tccacggcca atacagtggta tagaactaat catcagctag
1381 aaaatctgga agcagaaaact gtcgggttgc cctaacaggg tctcatgcca ttccgaccc
1441 caccaagctt agaagccacc atgtatgtgg aagcagggtt ctcaagaat gtgttaggagg
1501 ctctaattct ctaggaaagt gcctactttt aggtcatcca acctctttcc tctctggcca
1561 ctctgctctg cacatttagag ggacagccaa aagtaagtgg agcatttggaa agggaaaggaa
1621 tataccacac cgaggagttc agtttgc a agacacccag tggaaacaaa accccatcg
1681 gtatgtgaat tgaagtcatc ataaaaagggtt acccttctgt ctgttaagatt ttatttca
1741 gcaaatattt atgacctcaa caaagaagaa ccatttttgc ttaagttcac cgttagtaaca
1801 cataaagtaa atgttaccc tgcattaaagc accttgaatg gaaggccgaa gtctttttag
1861 tggggatgaa tccattattt tatttttagac tttaacttc aactttaaat
1921 tagcatctgg ctaaggcatc atttcaccc ccatttctgt gttttgtatt gtttaaaaaaa
1981 aataacatct ctttcatcta gtcataat tgcaaggaa gagattagca tgaaaggtaa
2041 tctgaaacac agtcatgtgt canctgtaga aaggttgcatt ctcgttgcact ncaaataact
2101 ccaaagagtc atcatggggg attttcattt cttaggctt cagtggttgc ttccctggaaat
2161 tc

600-1-266P
SEQ ID NO:6

FIGURE 3B

Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
1 5 10 15
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val
20 25 30
Asn Leu Ser His Leu Asp Gly Asn Leu Thr Asp Pro Cys Gly Pro Asn
35 40 45
Arg Thr Asn Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Ser
50 55 60
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
65 70 75 80
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
85 90 95
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
100 105 110
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val
115 120 125
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile
130 135 140
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu
145 150 155 160
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys
165 170 175
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys
180 185 190
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala
195 200 205
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser
210 215 220
His Pro Thr Trp Tyr Trp Glu Asn Leu Val Lys Ile Cys Val Phe Ile
225 230 235 240
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu
245 250 255
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu
260 265 270
Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
275 280 285
Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
290 295 300
Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
305 310 315 320
His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
325 330 335
Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
340 345 350
Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
355 360 365
Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
370 375 380
Thr Asn His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
385 390 395 400

FIGURE 4

SEQ ID NO:7

1 ggaattccgg ctataggcg aggagaatgt cagatgctca gctcggccc ctccgc
61 cgctcctctc tgtctagcc agactgggt tctgtaaac acagcaggag ctgtggc
121 ggccaaaggaa agcggtcgag gcgcttggaa cccgaaaagt ctcgggtctc ctggctac
181 cgcacagcg tggccccc ggcgtcagta ccattggacag cagcgtgcc cccacgaacg
241 ccagcaattt cactgtatcc ttggcgact caagttgtc cccagcaccc agccccgg
301 cctgggtcaa cttgtccac tttagatggca acctgtccga cccatgcggg cccgaaacc
361 ccaatctggg cgggagagac agcctgtgcc ctccgaccgg cagtccctcc atgatcac
421 ccatcacatgatggccctc tactccatcg tgcgttggt ggggtcttc gaaaaacttcc
481 tggcatgtatgtatgtc agatacacca agatgaagac tgccaccaac atctacattt
541 tcaacccctgc tctggcagat gccttagcca ccagtaccct gccttccag agtgtgaatt
601 acctaattggg aacatggcca ttggaaacca tcctttgcaaa gatagtgtatcc tccatagatt
661 actataacat gttcaccaggc atattcaccc tctgcaccat gagggtttgat cgatacattt
721 cagtctgcca ccctgtcaag gccttagatt tccgtactcc cccaaatgcc aaaattatca
781 atgtctgcaa ctggatccctc tcttcagccca ttggcttcc tggatgttca atggctac
841 caaaatacag gcaagggttcc atagattgtat cactaacatt ctctcatcca acctggact
901 gggaaaaacctt cgtgaagatc tggatgttca tcttcgcctt cattatgcca gtgc
961 ttaccgtgtg ctatggactg atgatcttgc gcctcaagag tgcgttgc ctctctgg
1021 ccaaagaaaa ggacagggat ctgcgaagga tcaccaggat ggtgttgc gttgggctg
1081 tggatgtatgtatgtc ctgctggact cccattcaca ttacgtcat cattaaagcc ttgg
1141 tcccgaaaac tacgttcccg actgtttttt ggcacttctg cattgtctca gttt
1201 acagctgcct caacccagtc ctttatgtat ttctggatga aaacttcaaa cgtatgttca
1261 gagagttctg tatcccaacc tcttccaaca ttgagcaaca aaactccact cgaattcg
1321 agaacactag agaccaccccc tccacggcca atacagtggat tagaactaat cat
1381 aaaatctgga agcagaaaact gtcgggtgc cctaacaggg tctcatgcca ttcc
1441 caccaagctt agaagccacc atgtatgtgg aagcaggtt cttcaagaat gtgt
1501 ctcttaattct ctagggaaagt gcctactttt aggtcatcca acctcttcc tctctgg
1561 ctctgttctg cacatttagag ggacagccaa aagtaagtgg agcatttggaa
1621 tataccacac cgaggagtcc agtttgc agacacccag tggaaacaaa acccatcg
1681 gtatgtgaat tgaagtcatc ataaaagggtt acccttctgt ctgt
1741 gcaaataattt atgacccatca caaagaagaa ccatctttt ttaagttcac cgt
1801 cataaaagttt atgctaccc tgcataaaggc accttgaatg gaaggccg
1861 tggatgttgc aggaaatgaa tccatttattt tatttttagac ttttacttca
1921 tagcatctgg ctaaggcatc attttcaccc ccatttcttgc gtttgc
1981 aataacatct ctttcatctc gtcataat tgcaaggaa gagatttagca
2041 tctgaaacac agtcatgtgt canctgttgc aaggttgc
2101 ccaaagagtc atcatggggg attttcattt cttaggctt cagtggttgc
2161 tc

SEQ ID NO:8

1 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcggtccc ctccgcctga
61 cgctcctctc tgtctcagcc aggactgggt tctgtaaaggaa acagcaggag ctgtggcagc
121 ggcgaaagga agcggctgag gcgcgttggaa cccgaaaagt ctcggtgctc ctggctacct
181 cgcacagcgg tgcccgcgg gccgtcagta ccatggacag cagcgtgccc cccacgaacg
241 ccagcaattg cactgatgcc ttggcgtact caagttgctc cccagcaccc agccccgggt
301 cctgggtcaa cttgtccac ttagatggca acctgtccga cccatgggt cccgaaaccgca
361 ccaacctggg cgggagagac agcctatgcc ctccgaccgg cagtcctcc atgatcacgg
421 ccatcacat catggccctc tactccatcg tgtgcgttgt ggggccttc ggaaacttcc
481 tggtcatgta tgtgattgtc agatacacca agatgaagac tgccaccaac atctacattt
541 tcaaccttgc tctggcagat gccttagcca ccagtacctt gccctccag agtgtgaatt
601 acctaattggg aacatggcca tttggaacca tcctttgcaaa gatagtgatc tccatagatt
661 actataaacat gttcaccaggc atattcaccc tctgcaccat gagtggtgat cgatacattt
721 cagtcgtcca ccctgtcaag gccttagatt tccgtactcc cccgaaatgcc aaaattatca
781 atgtctgcaa ctggatcctc tcttcagcca ttggctttcc tgtaatgttc atggctacaa
841 caaaatacag gcaagggtcc atagattgta cactaacatt ctctcatcca acctggtaact
901 gggaaaacact cgtgaagatc tgtgtttca tcttcgcctt cattatgcca gtgctcatca
961 ttaccgtgtc ctatggactg atgatcttgc gcctcaagag tgtccgcatt ctctctggct
1021 ccaaagaaaa ggacaggaat cttcgaagga tcaccaggat ggtgctgggt gtggggctg
1081 tggtcatcgat ctgctggact cccattcaca tttacgtcat cattaaagcc ttggttacaa
1141 tcccgaaaac tacgttccag actgtttctt ggcacttctg cattgtctca ggttacacaa
1201 acagctgcct caacccagtc ctttatgcat ttctggatga aaacttcaaa cgatgcttca
1261 gagagttctg tatcccaacc ttttccaaaca ttgagcaaca aaactccact cgaattcgtc
1321 agaacactag agaccacccc tccacggcca atacagtgga tagaactaat catcagctag
1381 aaaatctgga agcagaaaact gctccgttgc cctaacadggg tctcatgcca ttccgcaccc
1441 caccaggctt agaaggccacc atgtatgtgg aagcagggtt cttcaagaat gtgttaggagg
1501 ctctaattct ctagggaaagt gcctactttt aggtcatcca acctcttcc tctctggcca
1561 ctctgctctg cacatttagag ggacagccaa aagtaagtgg agcatttggaa aggaaaggaa
1621 tataaccacac cgaggagtcc agtttgcata agacacccag tggaaacaaa acccatcgat
1681 gtatgtgaat tgaagtcatc ataaaaagggtt acccttctgt ctgttaagatt ttattttca
1741 gcaaatattt atgaccccaa caaagaagaa ccatctttt ttaagttcac cgttagtaaca
1801 cataaagtaa atgctaccc tgcataaaggc accttgaatg gaaggccgat gtccttttag
1861 tggggatgaa tccattattt tatttttagac tttaacttc aacttaaaat
1921 tagcatctgg ctaaggcattt atttcacctt ccattttttt gttttgtatt gttaaaaaaa
1981 aataacatctt ctttcatcta gctccataat tgcaaggaa gagatttagca tggaaaggtaa
2041 tctgaaacac agtcatgtgt canctgtaga aaggttgatt ctcatgcact ncaaataactt
2101 ccaaagagtc atcatggggg attttcattt cttaggctt cagtggtttt gtcctggaaat
2161 tc

SEQ ID NO:9

1 ggaattccgg ctataggcag aggagaatgt cagatgctca gctcggtccc ctccgcctga
61 cgctcctctc tgtctcagcc aggactggtt tctgtaaagaa acagcaggag ctgtggcagc
121 ggcgaaagga agcggctgag ggcgttggaa cccgaaaagt ctcggtgctc ctggctacct
181 cgcacagcgg tgcccgcccc gccgtcagta ccatggacag cagcgtgcc cccacgaacg
241 ccagcaattg cactgatgcc ttggcgtact caagttgtct cccagcaccc agccccgggt
301 cctgggtcaa cttgtccccac ttagatggca acctgtccga cccatgcggg cccaaccgca
361 ccaacacctggg cgggagagac agcctgtgcc ctccgaccgg cqqcagtccctcc atgatcacgg
424 ccatcacqat catggccctc tactccatcg ttgtcgtggg ggggctcttc ggaaacttcc
484 tggtcatgtt tggattgtc agatacacca agatgaagac tgccaccaac atctacattt
544 tcaacacctgc tctggcagat gccttagcca ccagtaccct gcccttccag agtgtgaatt
604 acctaattggg aacatggcca tttggaaacca tccttgcaaa gatagtgatc tccatagatt
664 actataacat gttcacccaggc atattcaccc tctgcaccat gagtgttgcat cgatacatgg
724 cagtcgtccca ccctgtcaag gccttagatt tcgtactcc ccgaaatgcc aaaattatca
784 atgtctgca cttggatccctc tcttcagcca ttggcttcc tptaatgttc atggctacaa
844 caaaaatacag gcaagggtcc atagattgtt cactaacatt ctctcatcca acctggtaact
904 gggaaaaacct cgtgaagatc tggatgttca tcttcgcctt cattatgcca gtgctcatca
964 ttaccgtgtg ctatggactg atgatcttc gcctcaagag tggccatgcatg ctctctggct
1024 cccaaagaaaa ggacaggaat cttcgaagga tcaccaggat ggtgctgggt gtgggtggctg
1084 tggatcgatc ctgctggact cccattcaca tttacgtcat cattaaagcc ttggttacaa
1144 tcccgaaaac tacgttccag actgtttctt ggcacttctg cattgtctta ggttacacaa
1204 acagctgcct caacccagtc ctttatgcat ttctggatga aaacttcaaa cgatgcttca
1264 gagagttctg tatcccaacc tcttccaaca ttgagcaaca aaactccact cgaattcgtc
1324 agaacactag agaccacccc tccacggcca atacagtggta tagaactaat catcagctag
1384 aaaatctgga agcagaaaact gctccgttgc cctaacaggg tctcatgcca ttccgacctt
1444 caccaagctt agaagccacc atgtatgtgg aagcagggtt cttcaagaat gtgttaggagg
1504 ctctaattct ctaggaaagt gcctactttt aggtcatcca acctctttcc tctctggcca
1564 ctctgctctg cacatttagag ggacagccaa aagtaagtgg agcatttggaa aggaaaggaa
1624 tataccacac cgaggagtcc agtttgc agacacccag tggaaccaa acccatcgt
1684 gtatgtgaat tgaagtcatc ataaaaggtt acccttctgt ctgtaaagatt ttatttca
1744 gcaaatattt atgaccccaa caaagaagaa ccatttttgc ttaagttcac cgttagtaaca
1804 cataaagttt atgctaccctc tgatcaaagc accttgaatg gaaggtccga gtcttttttag
1864 tggatgttgc aaggaaatgaa tccattattt tatttttagac tttaacttc aactttaaaat
1924 tagcatctgg ctaaggcattc attttccactt ccatttcttg gttttgtatt gtttttttttt
1984 aataacatct ctttcatcta gctccataat tgcaaggaa gagattagca tgaaaggtaa
2044 tctgaaacac agtcatgtgt canctgtaga aaggttgatt ctcatgcact ncaaataactt
2104 ccaaagagtc atcatggggg atttttcattt ctttaggctt cagtggtttg ttccctggaaat
2164 tc

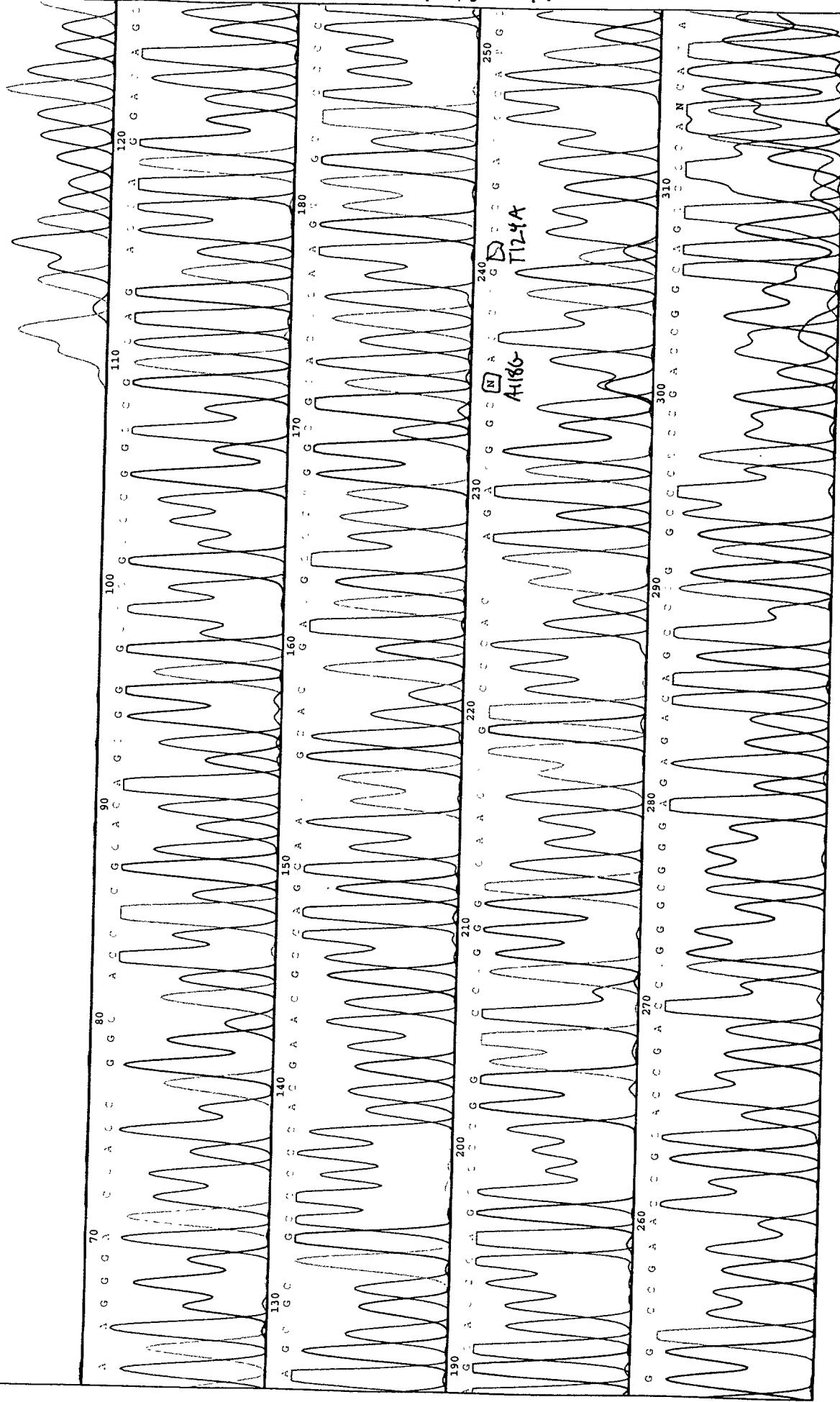
600-1-266P
SEQ ID NO:10

FIGURE 6B

Met Asp Ser Ser Ala Ala Pro Thr Asn Ala Ser Asn Cys Thr Asp Ala
1 5 10 15
Leu Ala Tyr Ser Ser Cys Ser Pro Ala Pro Ser Pro Gly Ser Trp Val
20 25 30
Asn Leu Ser His Leu Asp Gly Asn Leu Ser Asp Pro Cys Gly Pro Asn
35 40 45
Arg Thr Asn Leu Gly Gly Arg Asp Ser Leu Cys Pro Pro Thr Gly Gly Ser
50 55 60
Pro Ser Met Ile Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val
66 71 76 81
Cys Val Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val
86 91 96
Arg Tyr Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu
101 106 111
Ala Leu Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val
116 121 126
Asn Tyr Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile
131 136 141
Val Ile Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu
146 151 156 161
Cys Thr Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys
166 171 176
Ala Leu Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Ile Asn Val Cys
181 186 191
Asn Trp Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala
196 201 206
Thr Thr Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser
211 216 221
His Pro Thr Trp Tyr Trp Glu Asn Leu Val Lys Ile Cys Val Phe Ile
226 231 236 241
Phe Ala Phe Ile Met Pro Val Leu Ile Ile Thr Val Cys Tyr Gly Leu
246 251 256
Met Ile Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu
261 266 271
Lys Asp Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val
276 281 286
Ala Val Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile
291 296 301
Lys Ala Leu Val Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp
306 311 316 321
His Phe Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val
326 331 336
Leu Tyr Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe
341 346 351
Cys Ile Pro Thr Ser Ser Asn Ile Glu Gln Gln Asn Ser Thr Arg Ile
356 361 366
Arg Gln Asn Thr Arg Asp His Pro Ser Thr Ala Asn Thr Val Asp Arg
371 376 381
Thr Asn His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
386 391 396 401

;00-1-266 FIG 7B

Chromas 1.45 File: Q9938823 Sequence Name: Q9938823 Run ended: Sep 29, 1999 (E) Standard sequence - double heterozygote All 86, T1244 Page 1 of 2



600-1-266P FIG 81

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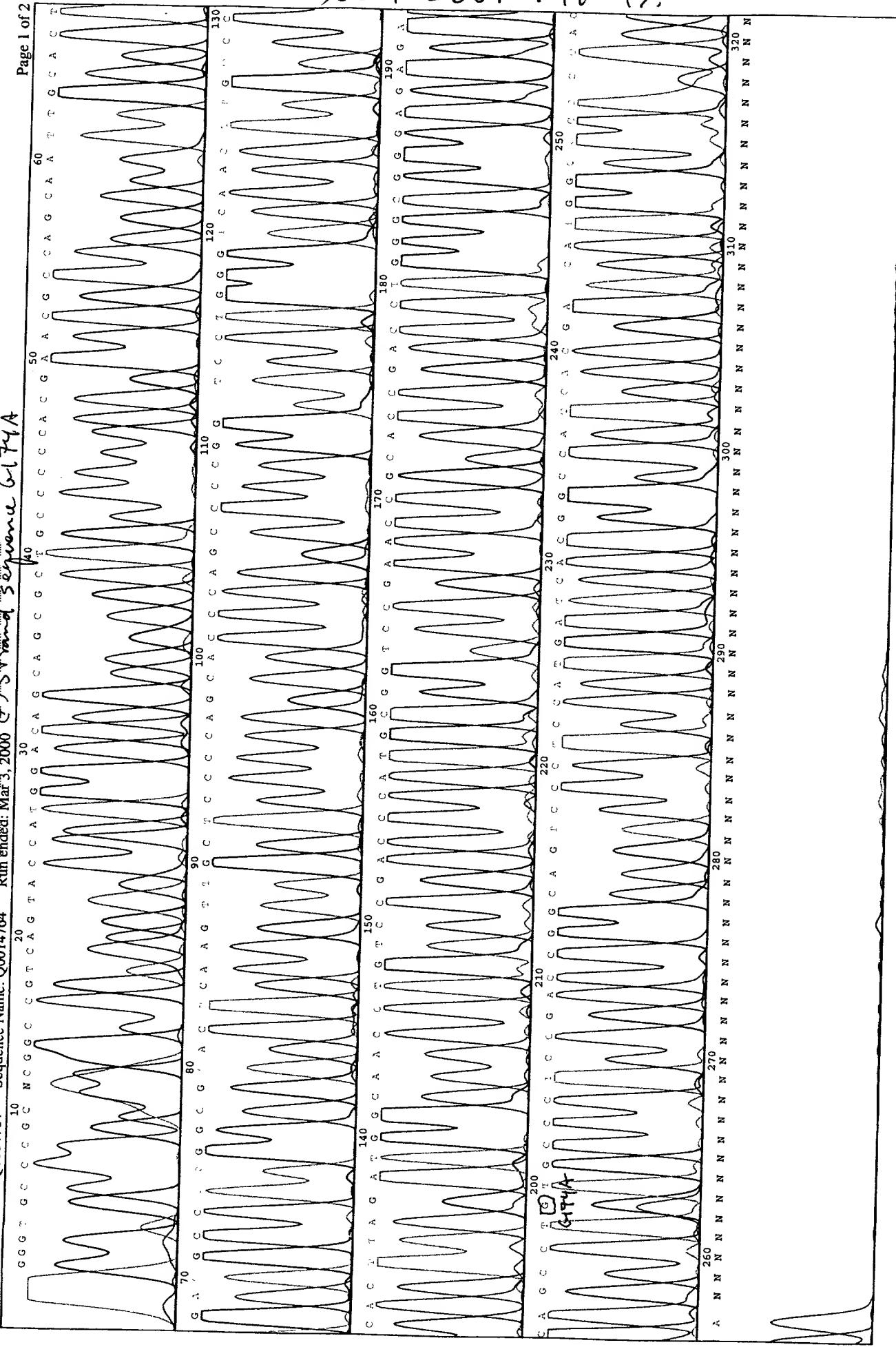
Chromas 1.45 File: Q0014861 Sequence Name: Q0014861 Run Ended Mar 3, 2000 (1) Grand sequence C153-T

00-1-266P FIG 9A

Chromas 1.45 File: Q0014764 Sequence Name: Q0014764

Run Ended: Mar 3 2000 10:35:50

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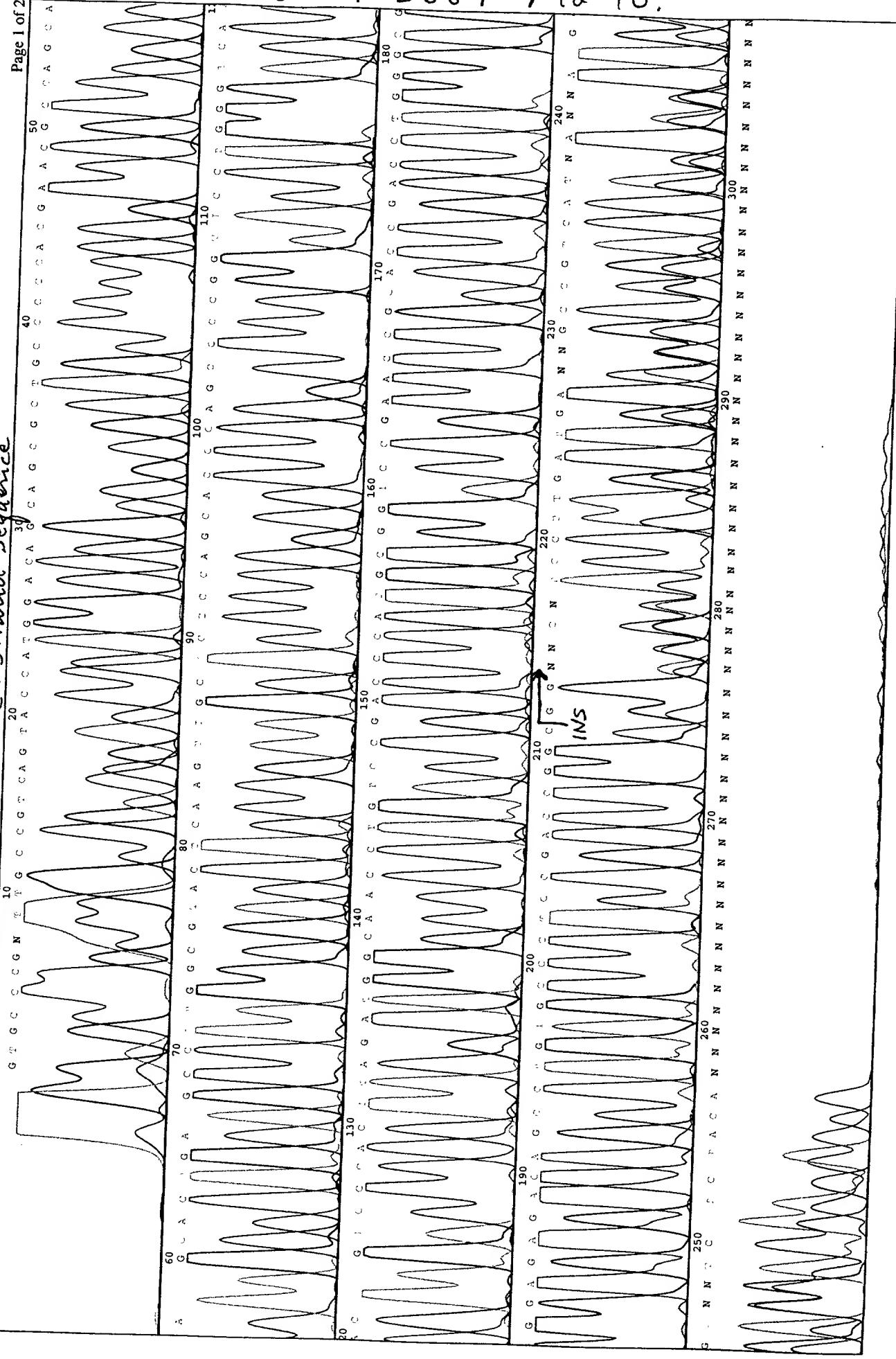


28

288

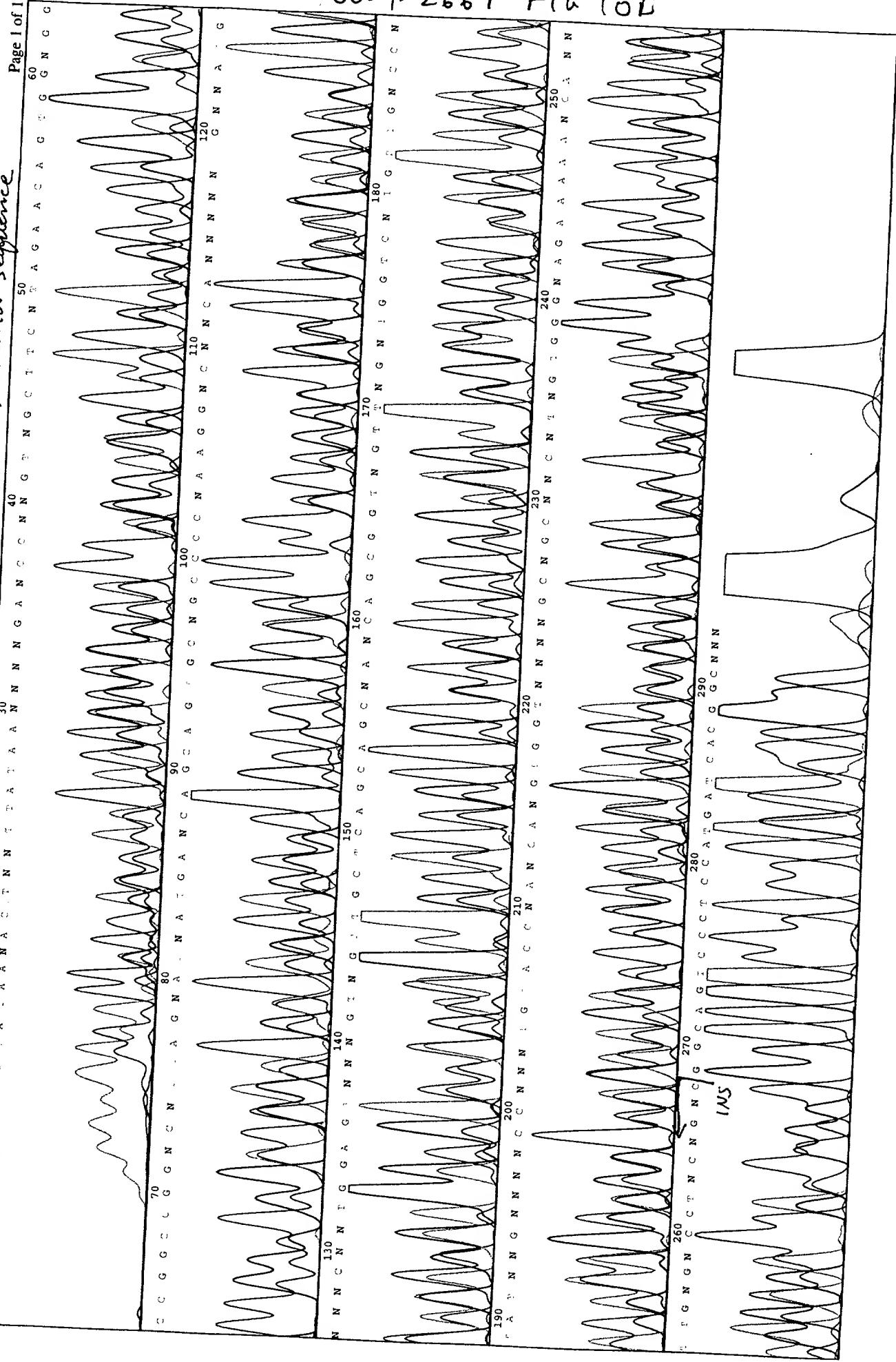
10

of 2 G / T-2667 FIG 10.



Chromas 1.45 File: Q0014871 Sequence Name: Q0014871 Submitted: Mar 3, 2006

00-1-266P FIG 10D



Chromas 1.45 File: Q0038503 Sequence Name: Q0038503 Run ended: May 30, 2000 ForumID 30

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Chromas 1.45 File: Q0038507 Sequence Name: Q0038507 Run ended: May 30, 2000 Reversal

N N N N N N N N N N N N N N N N N N N N

11

5

